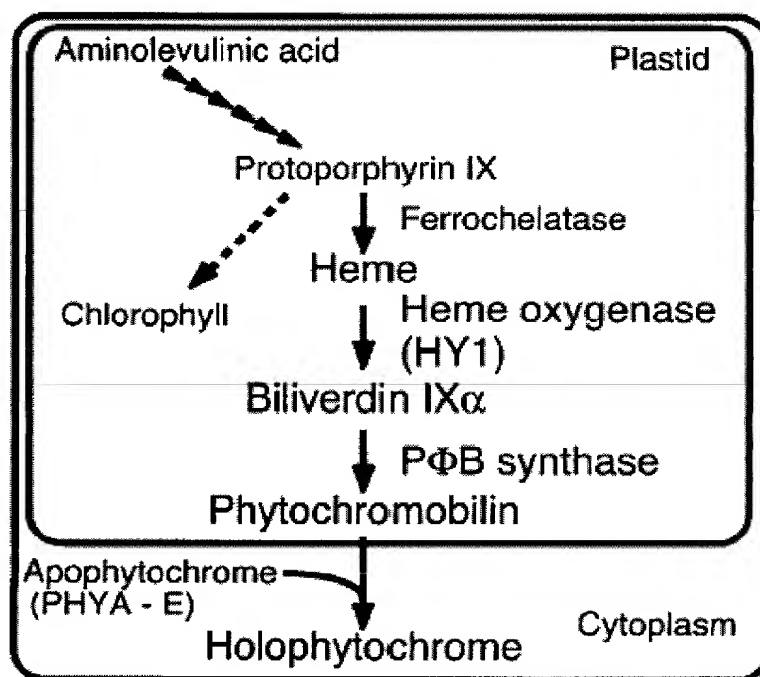
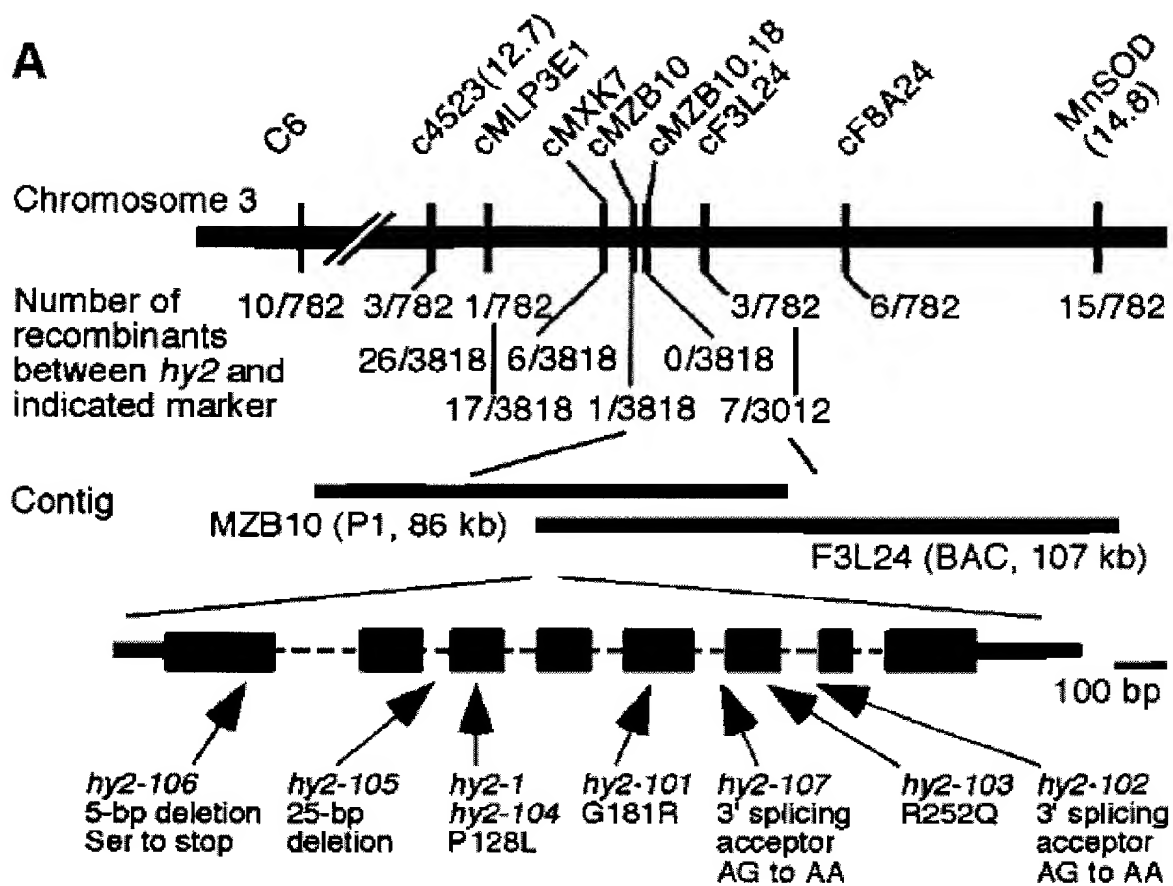


**Fig. 1**



**Fig. 2**

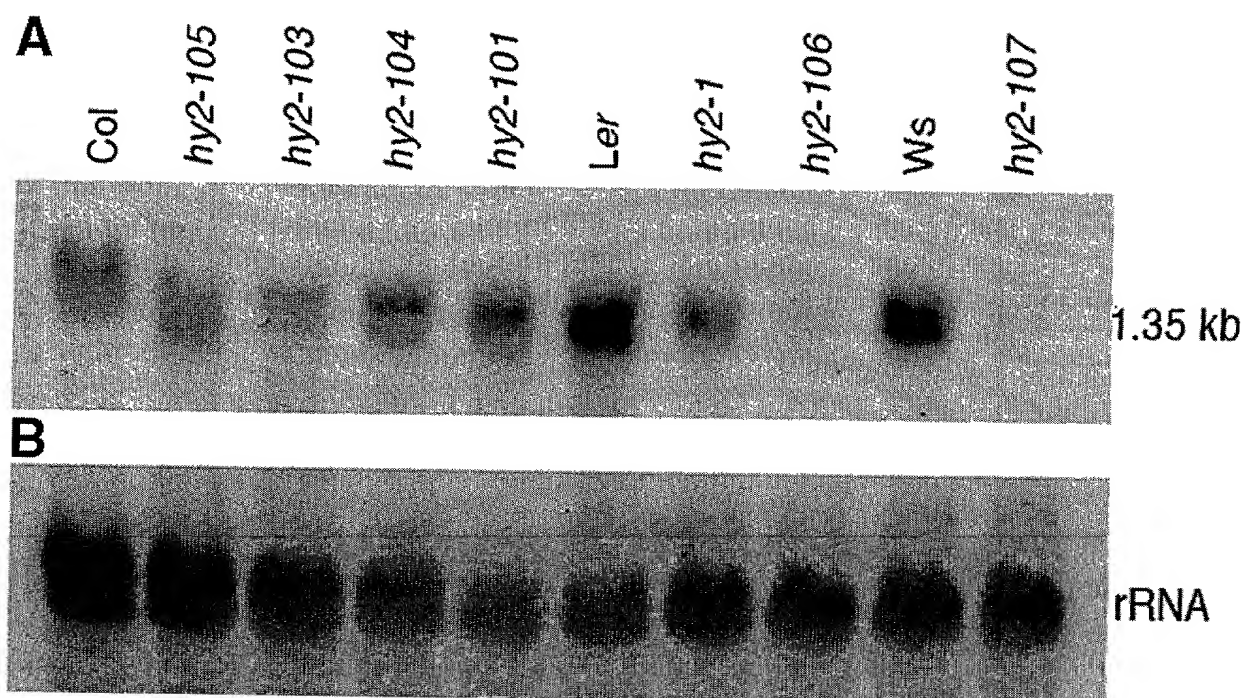


**Fig. 3A**

106250-106250

gaattcccccacgtcaacgtgactgtgcattccacgtggcggatgtgggocctatagttgg 60  
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aactgtgaaattttatctcttttatagataaAGAATCTTGCTTTTTCAGTTTTCAGTA 180  
TGAAGAAGAATTGAAGAGAGTGTCCGAGGAAGGAGACCTTTGGTTTCAGTTTGTGAGTCT 240  
TGTTGTAATGGCTTTATCAATGGAGTTTGGGTTTTCAAATTGGGTCATGCTTCAAGGCACC 300  
M A L S M E F G F S I G S C F K A P  
AAACCCACCTGTTTCTAATCTCTGCAAGCCCTAATAAGATCAATTTCACGTTGAGAAGGAG 360  
N P P V L I S A S P N K I N P T L R R R  
AAAGAAAAGATTCTTACTTAGAGTCTCTGCTGTGTCTGTATAGGAATTCGCAGAGTCTGC 420  
hy2-106 \*\*\*\*\*  
K K R F L L R V S A V S Y K E F A E S A  
TTTAGAAGAAACCAGGAAAGGATCGTTCTTGAACCTTCACATCTCCAGgtatatgcaat 480  
L E E T R K R I V L E P S H L Q  
tacatttgcttagtgtgaggattatatttctcattgtttcttgcgtgtgaattttg 540  
ggttaattgattttagttgtcattaggaacaaacaaataactttactgttatagactgc 600  
ttatataagtaaaagttcagattttgtttttctaatcagaaactgttttcagGAAAAGTA 660  
E K Y  
TAGTAGCATGACAGGACTAGATGGTAAGACCGAAGCTTCAAATGCTTGCTTTTAAATCTTC 720  
S S M T G L D G K T E L Q M L A F K S S  
AAAGATTAGACTCTTGAGGAGTATGGCAATAGAGAATGAGACAATGCAGgttttaacttca 780  
K I R L L R S M A I E N E T M Q  
gcagtaacaaactgattgttttagtcccatcttcoattactttcaattgattgattgtttgta 840  
hy2-105 \*\*\*\*\*  
tcttcgcttagGCTTTTGAAGTTTGGGGTTTCATGGAGCCTGAGTATGATACTCCCATAT 900  
hy2-1,hy2-10# T  
V F D F A G F H E P E Y D T P I F  
TCTGTGCTAACTTTTTCACATCTACCAACGTTAACATAGTTGTATTGtaagtttatcttct 960  
C A N F F T S T N V N I V V L  
agttatgctggagttatccaggtctgtattgtccaaactgatgttcaatattttactgtat 1020  
gttcttcttttagGACCTTAAATCCTTTGCATCAGTTGACTGACCAGACGGATTACCAAGA 1080  
D L N P L H Q L T D Q T D Y Q D  
CAAGTATTATAACAAGATAATGTCCATATATCACAAATATGCTGAGgtgaaccacaagaat 1140  
K Y Y N K I M S I Y H K Y A E  
acacaaaantactcaattgcaagtaaacctaattgctgaggtgtaaatgactgatcttgag 1200  
atttatttgcagACTTTCCCATGGGGAGGAAATTGACTGGTGAATCCATAAAGTTTTC 1260  
hy2-101 A  
T F P W G G K L T G E S I K F F  
TCGCCTTTGGTGATGTGGACTAGGTTTTCGTCTAGCAAAGAAAAACATAAGGCTTTGTTC 1320  
S P L V M W T R F S S S K E K H K A L F  
TCTCGGTTTCTAGAGTACTATCAGgtatataactcagggccaaaagcttaagggttttattg 1380  
S A F L E Y Y Q  
gaaactttgactgagaatctatcctcttcttctacagGCATGGCTTGAGATGACAATCC 1440  
hy2-107 a  
A W L E M T I Q  
AAGTGAGGGAGGAGATGGAACCATCTCATGTGAGAGCCAATTGTGAAGCACAACACAAGT 1500  
V R E E M E P S H V R A N C E A Q H K Y  
ACCTGACATGGCGAGCACAAAAGgtgatttccatttccgttttgtgtaatttgcattgtttga 1560  
hy2-103 A  
L T W R A Q K  
acagacactgtatctgtattgttacaatggatattgatttgggtgtttgcagGATCCTGGA 1620  
hy2-102 a  
D P G  
CATGGTCTTCTTAAAAGATTAGTAGGTGAAGCAAAGGCAAAGgtatataaaagatttgcac 1680  
H G L L K R L V G E A K A K  
cattagtgctcccatattatattagctttgtgaagatgttgaattgatttgaacaaatc 1740  
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E L L R D F L F N G V D E L G T K T F I  
TTGATTACTTTCCAGAGTACCAACAGAGATGGAAGCTGTAAGCGATAAACGAAGTATCA 1860  
D Y F P E Y Q T E D G T V S D K R S I I  
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G K S Y E T R P W D L T G Q F I G  
GATATATGTGAACAAGTCAGATTTCAGAGTCAACACAAAGAGGACGTGAACCTTAGGGA 1980  
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TTGTTTGAAGTACCATGCAATTGTAGTTTACAAAGTGTAGCTCTCAGCCCTTCATCAAAT 2100  
GAGAATCCTCGAGTATGATATGATTTTAAATGAAAATGTATTTCGTCTCTacctaatacaaca 2160

Fig. 3B



**Fig. 4A and Fig. 4B**

```

      *          20          40          60          80
M22 ARATH : MALSMHFCFSI GSCFARPYDEVLC SASFNKIMFTLRREKKRELETRAEVVEYKEFAEESALEETRXRIVLEESGQEKYSSNIGLQ GK- : 86
YCF2 SYNY : -----FTRFIMKELNSDITKK-----SGKGLWFPKGLKKCKKAKSS- : 86
YHF2 ECGM : -----KALMLQDLNNHKKKLI-ISKCKKINQVNGKMKKSKMKQ- : 40
YHF3 ECGM : -----MIIRKDSLSKELRWINTPTFMDIVDNL-SVFEIEVSASDFLQKESITIGSR : 34
YCF2 SYNY : -----MIDQRESDTFNHLGHSNUPFLQDAIKKL-EGLEVEITFPDFLQKESITIGSR : 34
SL0016 : -----KAVTDLELINSSELPFLRMIQQLALALAKSN-QSLEPKSQQFPELCIYEGRLSE : 36
      P          S

      *          100          120          140          160
M22 ARATH : -----TVKLMIAKXKNTLLESMARFN-XTQQVTFAGEMRPRITTFYCAFFYTSNVH--VUFGKMLNQITDCTDYQDKK : 106
YCF2 SYNY : -----SVVQSWLMDVQGVNMDVQRCALQUSQVPSAAYDYNHDCVYVLENGKAKKLLANQVQQLQQ---SKDVLDR : 116
YHF2 ECGM : -----TVKRLIMVPSQVNMVTRCALQKQQLSALAYENKQVLELLENGSLKKLLAVHSDQLQQ---KAKYPC : 116
YHF3 ECGM : RNFYVVTFTMAAKFERIDQVQACNGKSSQVFLHIDGNDVQVFAVYTLNPG--HLLHSDQKQNL--DNITENY : 137
YCF2 SYNY : SKSLPYVQATWACKIEKQVQALACSASAASTLFPVINDSQGLQVFGQVFFVAG--HLLHSDQKQNL--DNITENY : 137
SL0016 : -K--LVLENRCYQIFQKMHSLAKVSCDQLHCMTFEDLCLEFQCLLACFGC-VSAAALSSATQS---DRLQPAAR : 138
      A          R          G          P          Y          P          G          L          I          D          P

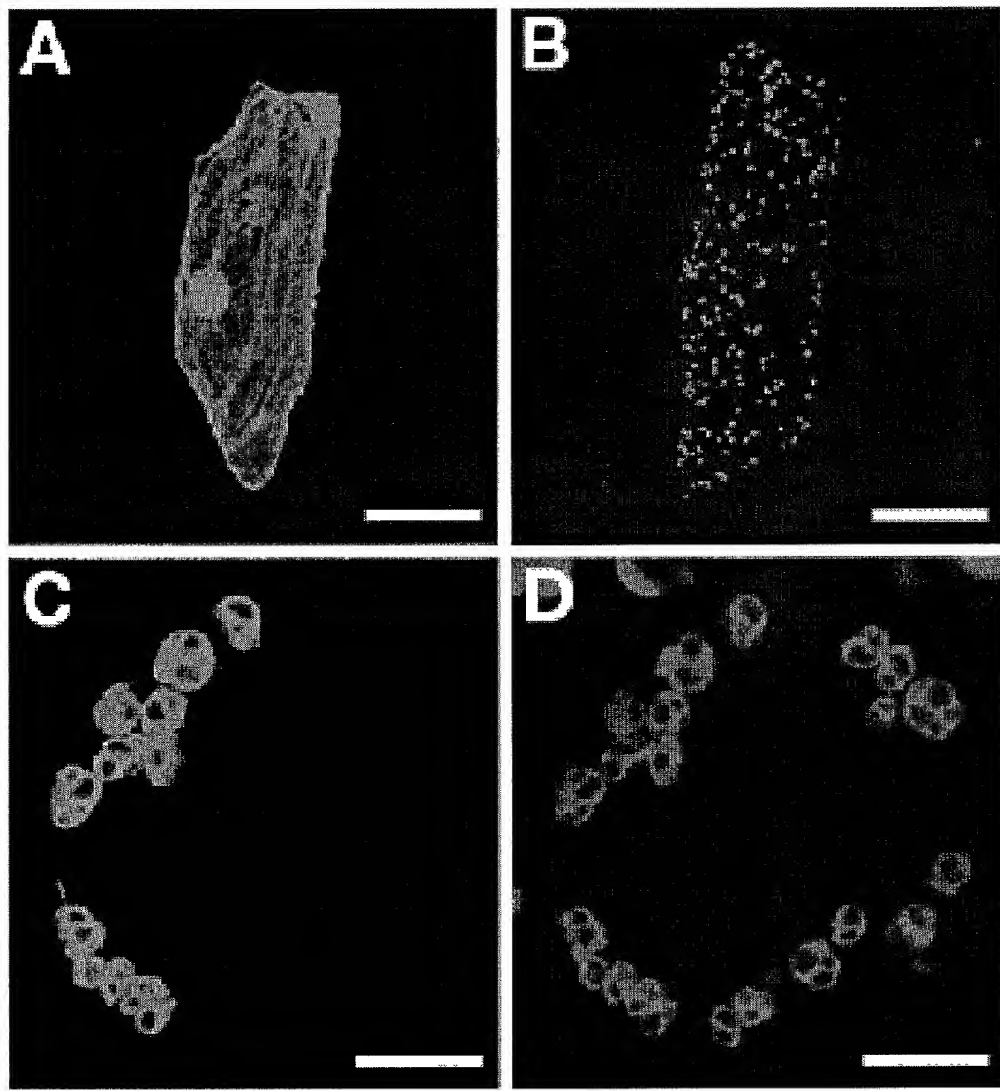
      *          180          200          220          240          260
M22 ARATH : KFM---S---YNNKAEIFENWSEKLGESINLEFLVLC---FSSSEKKKKAFAAELELYQALETIQVREEMIPSHVANCAL : 244
YCF2 SYNY : CCK---EIMQREPLNGERTMRSIDFNQDESKLQIC---CQATQQLSPELSSALMAADHDONKSTPSTIPPEVKNL : 193
YHF2 ECGM : DQD---LKNRQVDFNSQKIMKIDSNVSESPVLYN---GFFDLQCSALILDETHAWQNDKMSREYIRIIPSKVSL : 197
YHF3 ECGM : RLI---FTHUNQALLVQGNLFAKALFSSQVFLYPLSAKSDNILEMIFPAVQKSLGLELQNIKKFLAKH-ALKAL : 219
YCF2 SYNY : RLI---PFFERHQLQVYQPIPEEAQDEECFLVYPLSGEGDELQSIENPAENQDLGLEAARERERTER-SEVIL : 219
SL0016 : EDAELGQPEYEQQRELEPNS-----ETLSKYLIL---FKNVTEERFQGVVDLQIHCRQELVSEPEATAQ-TLKH : 208
      E          PS          S          SI

      *          280          300          320          340
M22 ARATH : FHKLLYTRADQGGGELRLVFNAAKALQRPFGQVDNLQKQVADVFVFFQKQKQGVSDKRSIIGKSYNTRPWLTCQPIG : 320
YCF2 SYNY : LKNDIISAKQAGGQFTSEKQDSSNRQHEPSSASSHK----- : 236
YHF2 ECGM : NIMQDLSAKQAGGQPSYKQCTACGQREPPSPESHVAD----- : 241
YHF3 ECGM : KKAHNNKSTQADAMLCREKSTEDNKKVLEMI----- : 257
YCF2 SYNY : RRYCDERAKQARQMTREHSETEAHTHTVQDL----- : 257
SL0016 : VTHCCQQQKQNDKTRNLEKKEFAAYKAKSQVLDVTD----- : 248
      G          V          D          P          E          G          W          E          L          F

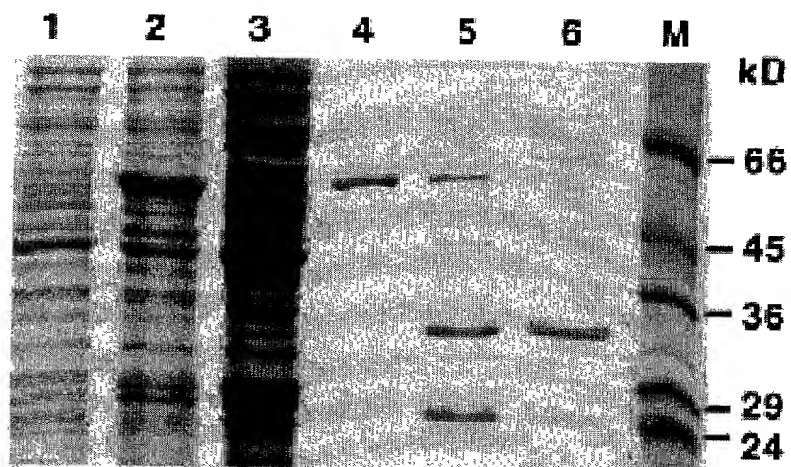
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Fig. 5

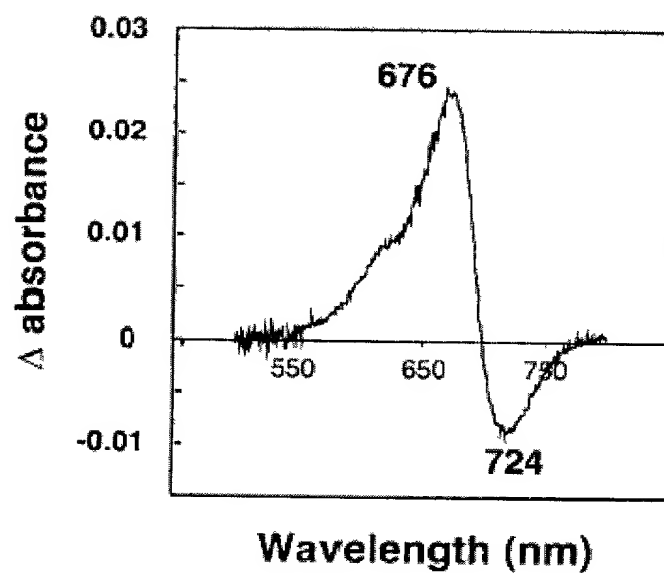
202405-09004



**Fig. 6A - 6D**

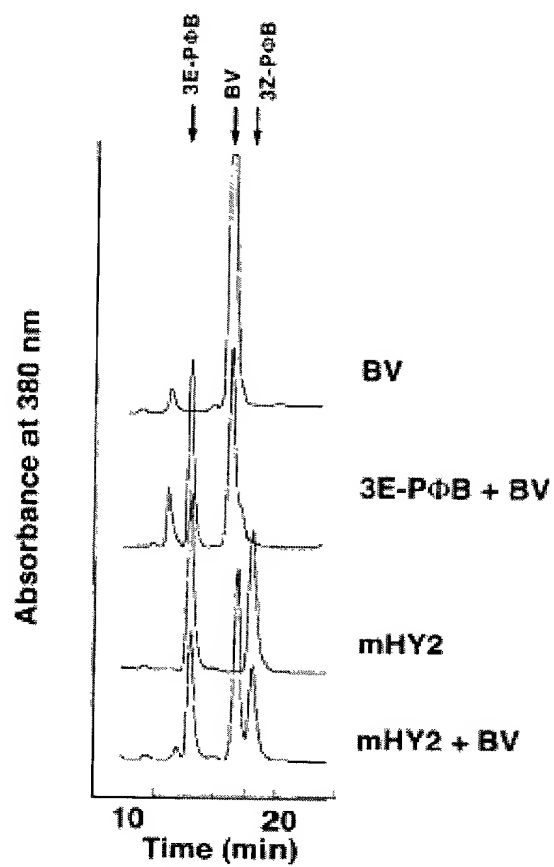


**Fig. 7**



**Fig. 8**





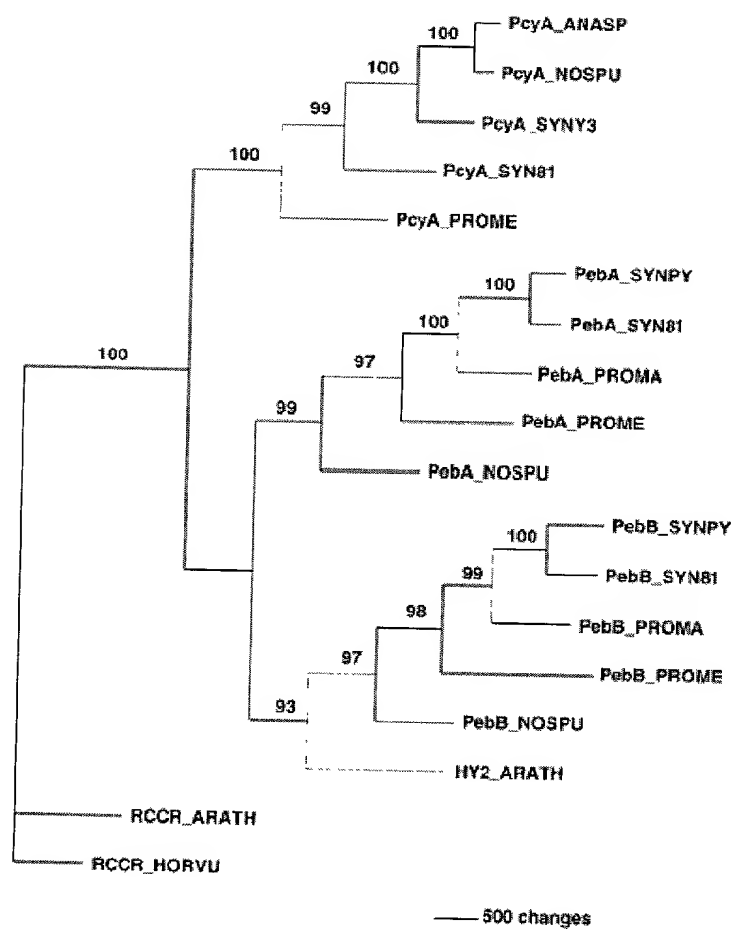
**Fig. 9**

	*	20	*	40	*	60	*	80	*	
PCYA_ANASP	:	---	---	---	---	---	---	---	---	43
PCYA_NOSPU	:	---	---	---	---	---	---	---	---	43
PCYA_SYN3	:	---	---	---	---	---	---	---	---	46
PCYA_SYN81	:	---	---	---	---	---	---	---	---	42
PCYA_PROME	:	---	---	---	---	---	---	---	---	44
Peba_SYN81	:	---	---	---	---	---	---	---	---	27
Peba_PROMA	:	---	---	---	---	---	---	---	---	31
Peba_PROME	:	---	---	---	---	---	---	---	---	25
Peba_NOSPU	:	---	---	---	---	---	---	---	---	64
Pebb_SYN3	:	---	---	---	---	---	---	---	---	44
Pebb_SYN81	:	---	---	---	---	---	---	---	---	45
Pebb_PROMA	:	---	---	---	---	---	---	---	---	44
Pebb_PROME	:	---	---	---	---	---	---	---	---	40
Pebb_NOSPU	:	---	---	---	---	---	---	---	---	37
HY2_ARATH	:	---	---	---	---	---	---	---	---	77
RCCR_ARATH	:	---	---	---	---	---	---	---	---	90
RCCR_HORVU	:	---	---	---	---	---	---	---	---	4

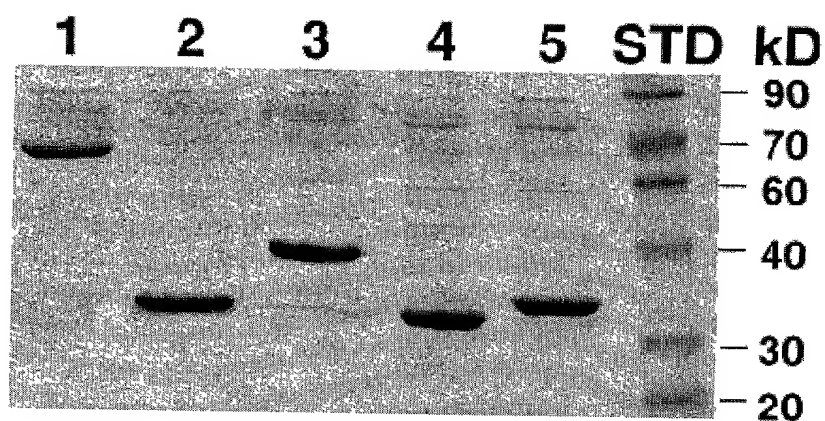
	*	100	*	120	*	140	*	160	*	180
PCYA_ANASP	:	---	---	---	---	---	---	---	---	126
PCYA_NOSPU	:	---	---	---	---	---	---	---	---	126
PCYA_SYN3	:	---	---	---	---	---	---	---	---	129
PCYA_SYN81	:	---	---	---	---	---	---	---	---	123
PCYA_PROME	:	---	---	---	---	---	---	---	---	127
Peba_SYN81	:	---	---	---	---	---	---	---	---	109
Peba_PROMA	:	---	---	---	---	---	---	---	---	109
Peba_PROME	:	---	---	---	---	---	---	---	---	113
Pebb_NOSPU	:	---	---	---	---	---	---	---	---	147
Pebb_SYN3	:	---	---	---	---	---	---	---	---	131
Pebb_SYN81	:	---	---	---	---	---	---	---	---	132
Pebb_PROMA	:	---	---	---	---	---	---	---	---	131
Pebb_PROME	:	---	---	---	---	---	---	---	---	127
Pebb_NOSPU	:	---	---	---	---	---	---	---	---	124
HY2_ARATH	:	---	---	---	---	---	---	---	---	159
RCCR_ARATH	:	---	---	---	---	---	---	---	---	181
RCCR_HORVU	:	---	---	---	---	---	---	---	---	66

Fig. 10

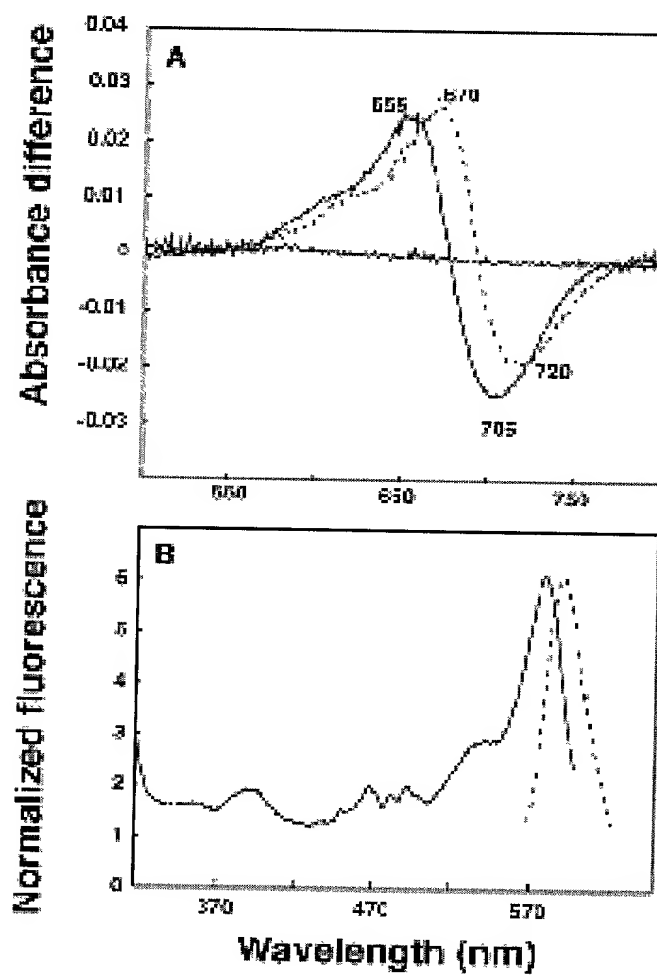




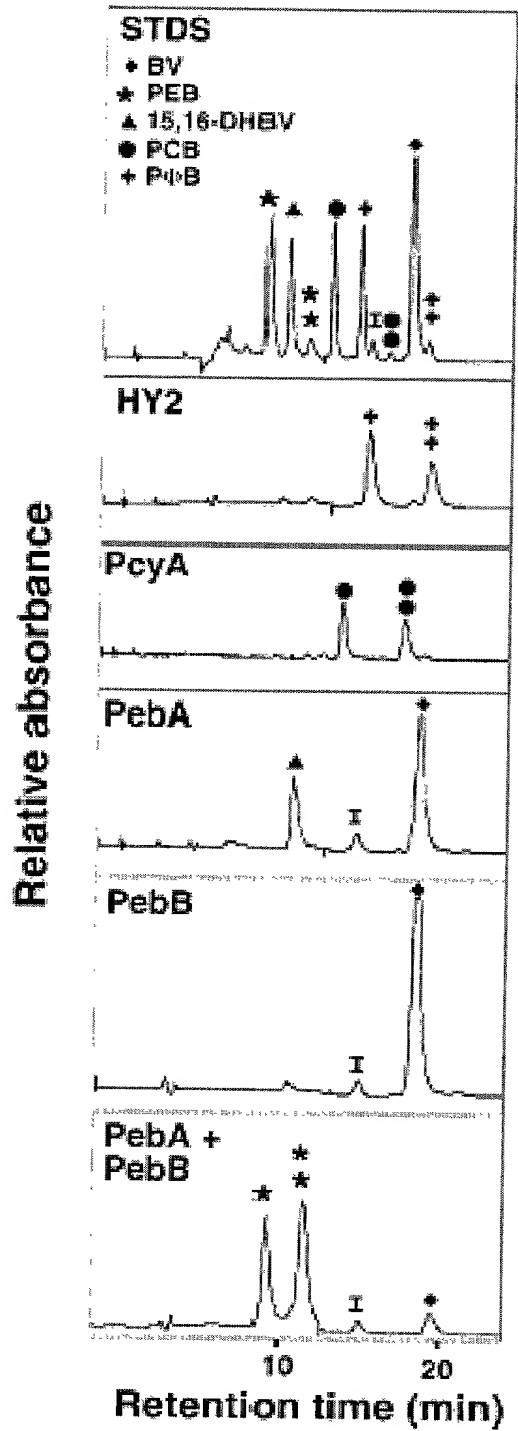
**Fig. 11**



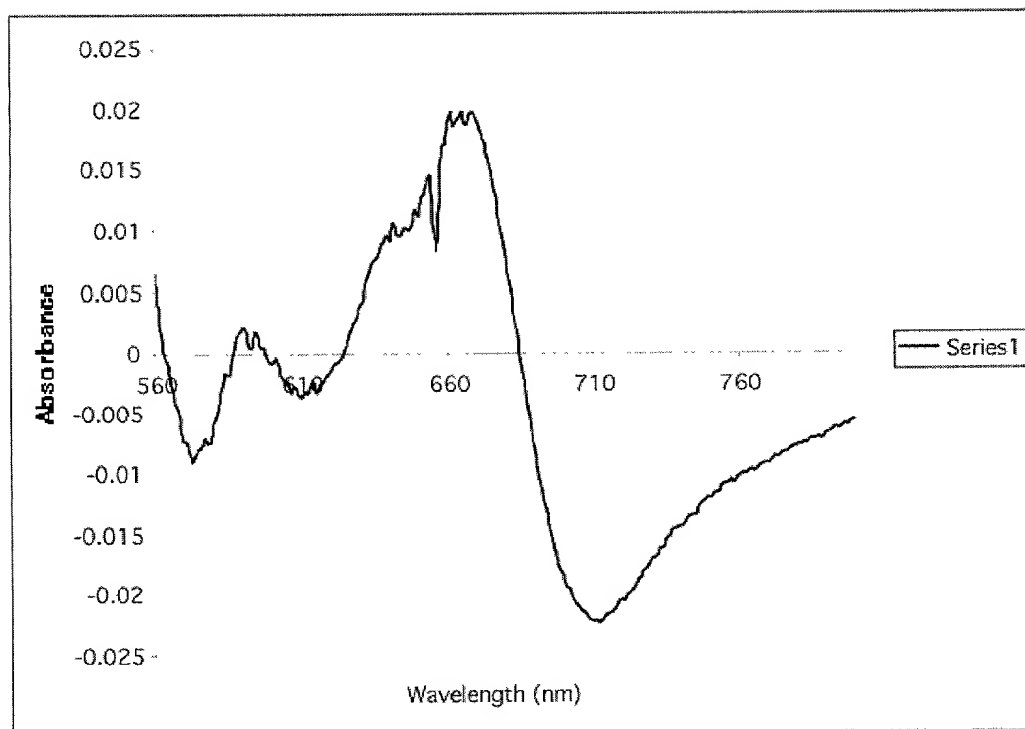
**Fig. 12**



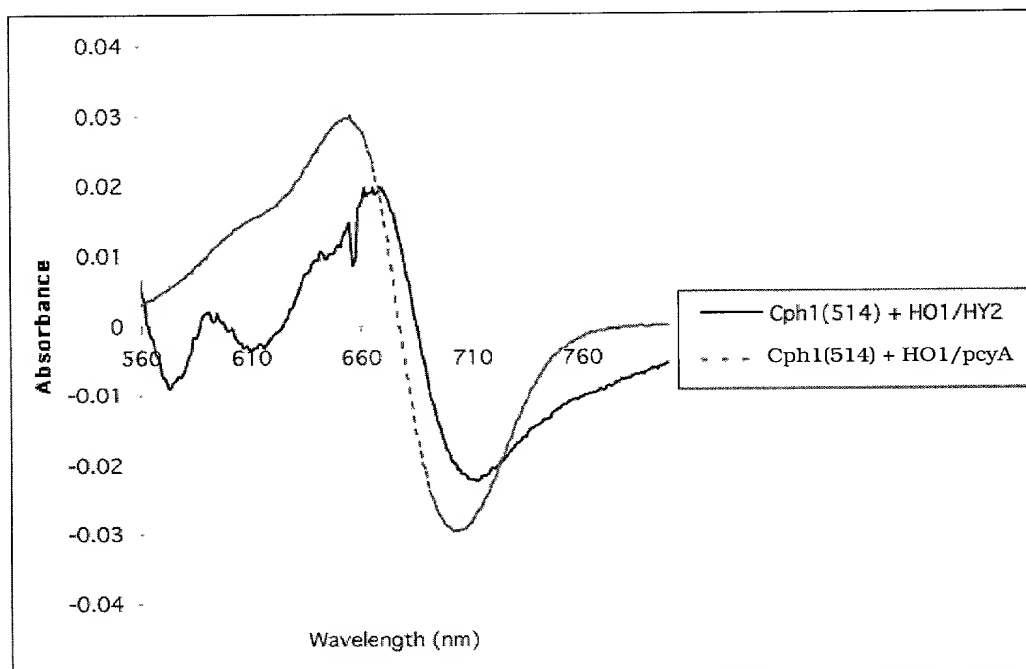
**Fig. 13A and 13B**



**Fig. 14**



**Fig. 15**



**Fig. 16**